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Research Article

Monotropa callistoma (Ericaceae), a new species based on morphological and molecular evidence from Hunan, China

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Abstract

The subfamily Monotropoideae (Ericaceae) comprises unique non-photosynthetic and mycoheterotrophic plants. Their extensive morphological reduction often poses significant challenges for species delimitation. In this study, we investigated an unknown *Monotropa* taxon collected from Hunan Province, China, through an integrative approach combining detailed morphological observation and phylogenetic analysis. We sequenced it, assembled the complete plastid genome and reconstructed phylogenetic trees using both chloroplast genomes and the nrITS region. Morphologically, this new entity is readily distinguished from its congener, *Monotropa uniflora*, by several key characteristics: 4–5 glabrous petals apically one-quarter orange and basally three-quarters white, 8–10 stamens with glabrous filaments, a nodding berry at maturity and a distinctly earlier flowering period (March–June vs. June–October). Phylogenetic reconstructions, based on both chloroplast genomes and nrITS data, consistently resolved this unknown taxon as a distinct lineage, clearly separating it from *M. uniflora* with strong support. Integrating evidence from morphology, phylogeny and phenology, we hereby describe it as a new species, *Monotropa callistoma*.

Key words: Ericaceae, *Monotropa*, morphology, new species, phylogeny, taxonomy

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Introduction

The subfamily Monotropoideae represents a unique lineage within the Ericaceae, being the only mycoheterotrophic and non-photosynthetic group amongst its nine subfamilies (Kron 1996; Kron et al. 2002; Liu et al. 2014). Members of this subfamily share a predominantly herbaceous habit, reduced embryos and a fully mycoheterotrophic and non-photosynthetic lifestyle, which has led to pronounced morphological reduction (Kron et al. 2002) and extensive loss of chloroplast genes (Logacheva et al. 2016; Braukmann et al. 2017; Liu et al.

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2020). The subfamily currently comprises two tribes and twelve genera (Rose and Freudenstein 2014; Liu et al. 2017; Zhao et al. 2018; Freudenstein and Broe 2024). In recent years, several new species have been discovered in East Asia (Wu et al. 2016; Suetsugu et al. 2023), suggesting that its diversity may be underestimated. As of 2025, 19 species have been formally recognised (POWO 2025).

During a field survey in Xinning County, Hunan Province in March 2021, we encountered an unusual *Monotropa* population. Subsequent investigations from 2022 to 2025 included repeated observations of several populations across the Province. A thorough review of herbarium records and literature confirmed that its morphology is distinct from all three known species in the genus. Amongst these three species, *Monotropa brittonii* Small and *Monotropa coccinea* Zucc. are distributed only in the Americas, while *Monotropa uniflora* L. is widely distributed in East Asia and North America (Table 1). Although *M. uniflora* is morphologically most similar to the present species, significant differences exist in petal colour, indumentum, number of petals, number of stamens, filament pubescence, style length and fruit type. Similarly, *Monotropastrum humile* (D.Don) H.Hara, also widespread in East Asia, shows morphological affinities, but differs in petal colour, indumentum and style length. Phylogenetic analyses, based on nrITS and complete chloroplast genome sequences, strongly support its taxonomic distinction. Integrating morphological, phylogenetic and phenological evidence, we here recognise it as a new species of *Monotropa* (Ericaceae).

Methods and materials

Taxon sampling and data collection

Our sampling encompassed 11 of the 12 recognised genera within subfamily Monotropoideae, with the exception of *Cheilotheca* Hook.f. *Arbutus unedo* L. and *Vaccinium macrocarpon* Aiton were selected as outgroups, based on prior research (Braukmann et al. 2017; Rose et al. 2018; Freudenstein and Broe 2024). Forty-three nuclear ribosomal internal transcribed spacer (nrITS) region and 17 chloroplast (cp) whole genomes were downloaded from NCBI and six nrITS and seven chloroplast whole genomes were newly sequenced (*Sarcodes* Torr. and *Pleuricospora* A.Gray only have nr dataset, no cp dataset). Two samples of *Monotropa callistoma* were derived from the type (PE02432010) and other (PE02432009) specimens collected during our fieldwork. In addition, we newly sequenced five accessions of the tribe Monotropeae from the PE Herbarium, including *Monotropa uniflora* L. (1 sample, China), *Monotropastrum humile* (D. Don) H. Hara (1 sample, Japan), *Hypopitys monotropa* Crantz (1 sample, China) and *Pterospora andromedea* Nuttall (2 samples, USA). Detailed collection information for all samples is provided in Suppl. material 1: table S1.

DNA extraction, amplification and sequencing

Total genomic DNA was extracted from approximately 20–30 mg of silica-gel-dried plant material using the standard CTAB (cetyl trimethylammonium bromide) method (Doyle et al. 1987). The quality-checked DNA samples were randomly sheared using a Covaris ultrasonicator to construct sequencing libraries. The library preparation workflow included end repair, A-tailing, adapter ligation, purification and

Table 1. Distribution of existing tribes, genera and species within Subfamily Monotropoideae. Species occurring in East Asia are highlighted in bold; those included in this study are marked with an asterisk (*).

Tribe	Genus		Species		Distribution
Tr. Pterosporeae Baill. (1891)	1	*Pterospora* Nutt.	1	*Pterospora andromedea* Nutt. *	Alaska to Mexico
	2	*Sarcodes* Torr.	1	*Sarcodes sanguinea* Torr. *	W. U.S.A. to NW. Mexico
Tr. Monotropeae Dumort. (1829)	3	*Pleuricospora* A.Gray	1	*Pleuricospora fimbriolata* A.Gray *	W. Canada to W. U.S.A.
	4	*Monotropastrum* Andres	2	***Monotropastrum humile* (D.Don) H.Hara ***	Himalaya to Russian Far East and Temp. E. Asia, Indo-China, N. Sumatera
				***Monotropastrum kirishimense* Suetsugu**	Japan (Honshu, Kyushu)
	5	*Eremotropa* Andres	1	***Eremotropa sciaphila* Andres ***	S. Central China
	6	*Monotropsis* Schwein. ex Elliott	2	*Monotropsis odorata* Schwein. *	SE. U.S.A
				Monotropsis reynoldsiae (A.Gray) A.Heller	N. & Central Florida
	7	*Allotropa* Torr. & A.Gray	1	*Allotropa virgata* Torr. & A.Gray *	W. Canada to W. U.S.A
	8	*Hemitomes* A.Gray	1	*Hemitomes congestum* A.Gray *	W. Canada to W. U.S.A
	9	*Pityopus* Small	1	*Pityopus californicus* (Eastw.) H.F.Copel. *	Washington to California
	10	*Monotropa* L.	3	*Monotropa brittonii* Small	SE. North Carolina to Florida
				Monotropa coccinea Zucc.	Mexico to Colombia
				***Monotropa uniflora* L. ***	N. Pakistan to Russian Far East and Japan, Canada to Mexico
	11	*Hypopitys* Hill	1	***Hypopitys monotropa* Crantz ***	Temp. Northern Hemisphere to Central America
	12	*Cheilotheca* Hook.f.	4	***Cheilotheca crocea* L.Wu & Yan Liu**	China (Guangxi)
				Cheilotheca khasiana Benth. & Hook.f.	Assam (Meghalaya)
				Cheilotheca malayana Scort. ex Hook.f.	Peninsula Malaysia (Perak)
				Cheilotheca sleumerana H.Keng	Sumatera

PCR amplification. The constructed libraries were initially quantified using Qubit 2.0 and the insert size was checked with an Agilent 2100 Bioanalyzer. Libraries with the expected insert size were then accurately quantified using quantitative PCR (Q-PCR) to ensure quality. Qualified libraries were pooled in appropriate proportions, based on effective concentration and the desired data volume, followed by cluster generation on the cBOT system. Sequencing was performed on the Illumina NovaSeq 6000 platform to generate 5–8 Gb of raw data per sample.

The raw reads were processed with fastp (Chen et al. 2018) to remove adapters and low-quality sequences, yielding clean data for subsequent assembly (see Suppl. material 1: table S2 for sequencing statistics). The nrITS region (ITS1-5.8S–ITS2-26S) and the complete chloroplast genome were assembled from the clean data using GetOrganelle v.1.7.1a (Jin et al. 2020). The assembled chloroplast genome was annotated using the Plastid Genome Annotator (PGA) (Qu et al. 2019) with the reference of *Monotropa uniflora* (NC_035582). The annotation was subsequently imported into Geneious v.2023.0.4 (Kearse et al. 2012) for manual verification and refinement. All sequence data utilised in our analyses are readily accessible in GenBank (Suppl. material 1: table S1).

Phylogenetic analyses

Phylogenetic relationships were reconstructed using two datasets: the nuclear ribosomal internal transcribed spacer (nrITS) region (49 sequences) and 23 single-copy coding sequences (CDSs) extracted from 24 chloroplast (cp) genomes.

The nrITS sequences and 23 cp-CDS were aligned separately using MAFFT v.7.221 (Katoh and Standley 2013). The alignments were manually inspected in

MEGA7 (Kumar et al. 2016) and subsequently refined using trimAl (Capella-Gutiérrez et al. 2009). The best-fit nucleotide substitution models, selected under the Akaike Information Criterion (AIC) by MrModelTest v.2.4 (Posada and Crandall 1998), were GTR+G for the nrITS dataset and GTR+I+G for the cp dataset.

Maximum Likelihood (ML) analyses were conducted with RAxML v.8.2.12 (Stamatakis 2014), with branch support assessed from 1000 bootstrap replicates. Bayesian Inference (BI) was performed using MrBayes v.3.2.7 (Ronquist et al. 2012), running two independent Markov Chain Monte Carlo (MCMC) analyses for one million generations each, with trees sampled every 1000 generations. The first 25% of sampled trees were discarded as burn-in. The consensus phylogenetic trees were visualised in FigTree v.1.4.4(available at: http://tree.bio.ed.ac.uk/software/figtree/).

Results

Morphological comparisons

This new species (Figs 1, 2) differs from its congener, *Monotropa uniflora*, by its petals (4 or 5, glabrous, apically one-quarter orange and basally three-quarters white vs. 5 or 6, white and typically densely villous on the inner surface in *M. uniflora*), stamens (8–10 with glabrous filaments vs. commonly 10 with pubescent filaments), earlier flowering period (starting from March vs. starting from June) and baccate fruit with parietal placentation, 1-loculed (vs. capsular fruit with axile placentation, 5-loculed). This species is also quite similar to *Monotropastrum humile* (D.Don) H.Hara, but can similarly be distinguished by corolla colour, pubescence and stamen length. A detailed morphological comparison is presented in Table 2 and the key to the species of *Monotropa* s.s. and *Monotropastrum*.

Chloroplast genome features of *Monotropa callistoma* and related species

Our results demonstrate a pronounced reduction in chloroplast genome size and gene content across the non-photosynthetic subfamily Monotropoideae (Table 3). The seven newly-sequenced chloroplast genomes ranged from ~ 34 kbp (*Hypopitys monotropa*) to ~ 49 kbp (*Pterospora andromedea*) and encoded 35 genes (*Hypopitys monotropa*) to 47 genes (*Monotropa uniflora*). The chloroplast genome of the new species, *Monotropa callistoma*, was assembled to a length of 41,041–41,085 bp and was annotated with 44 genes. It lacks several typical chloroplast genes, including trnM-CAT (and its copy) as well as trnF-GAA, reflecting the ongoing gene loss associated with the transition to a heterotrophic lifestyle in this lineage.

Phylogenetic analyses

Both phylogenetic reconstructions (Figs 3, 4) strongly supported *Monotropa callistoma* as a monophyletic lineage (PP = 1.00, BS = 100 in both datasets), which was placed within the genus *Monotropa* and resolved as sister to its type species, *M. uniflora*, with high support (PP = 1.00, BS = 100 in the plastome tree; PP = 1.00, BS = 98 in the nrITS tree).

Figure 1. Habitat and flowering habit of *Monotropa callistoma*. Photographed by Ze Wei.

In the nrITS phylogeny (Fig. 3), all eleven sampled genera formed well-supported monophyletic groups. This result corroborates previous taxonomic proposals to resurrect *Eremotropa* (Zhao et al. 2018) and retain *Hypopitys* (Liu et al. 2017; Freudenstein and Broe 2024). The tribe Monotropeae was divided into three major clades. Within the clade containing *Monotropa*, the genus was most closely related to *Monotropastrum*, followed successively by *Eremotropa* and *Monotropsis*. This intergeneric relationship was also supported by the chloroplast phylogeny (Fig. 4).

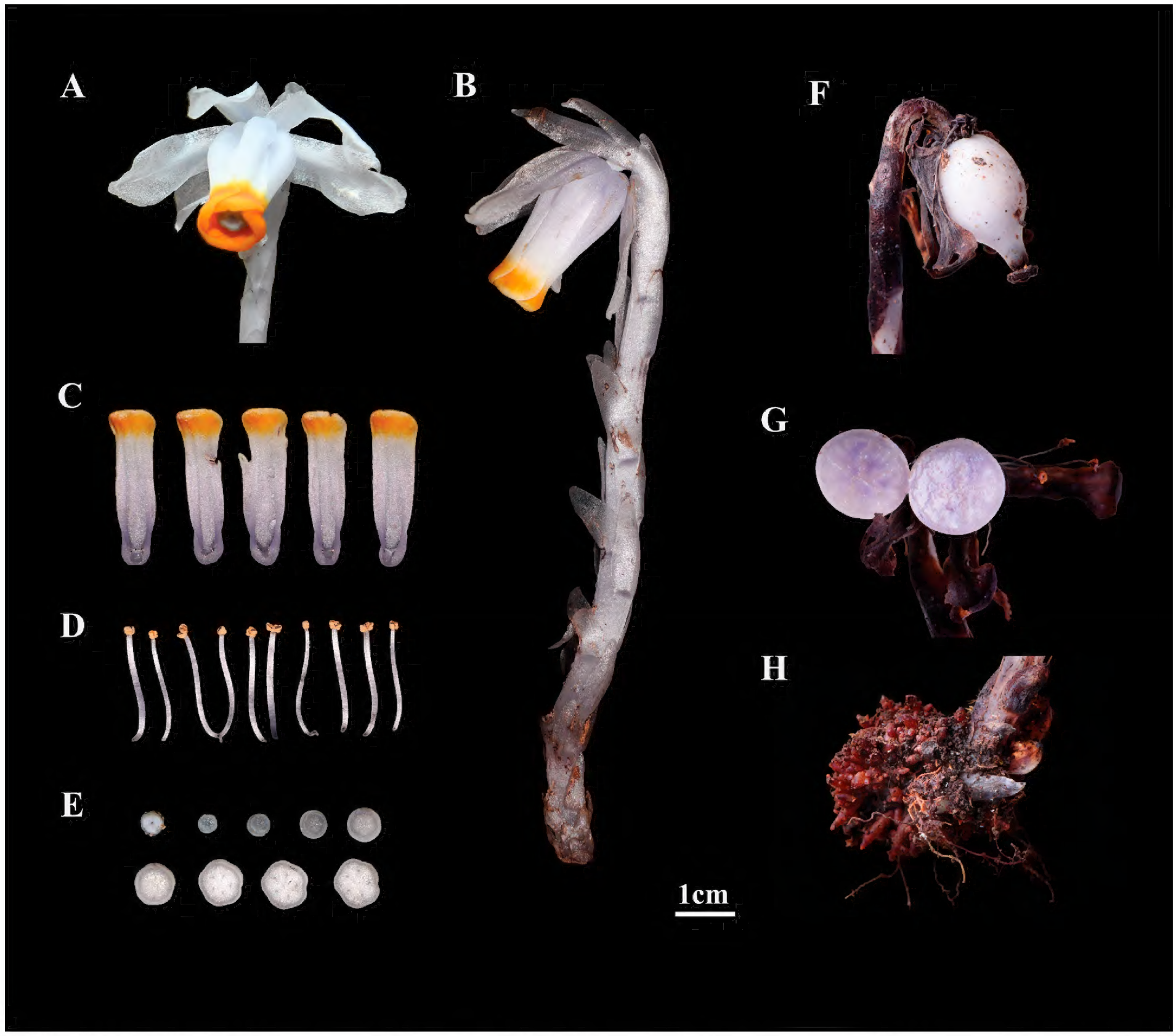

Figure 2. Morphology of *Monotropa callistoma*. **A.** Flower; **B.** Flowering plant showing scale-like leaves; **C.** Petals; **D.** Stamens; **E.** Transverse section of the ovary; **F, G.** Baccate fruit (berry) and its transverse section showing the parietal placentation; **H.** Mycorrhiza. **B–E.** Photographed by Zi Wang and others photographed by Ze Wei.

Table 2. Morphological comparison between *Monotropa uniflora*, *Monotropastrum humile* and *Monotropa callistoma* sp. nov.

Character	*Monotropa uniflora*	*Monotropa callistoma*	*Monotropastrum humile*
Petals	5–6, distinct, cuneate or obovate-oblong, 1.2–1.6 cm long, 5.5–7 mm wide at the broadest apex, margin irregularly toothed, inner surface often densely villous, caducous.	4–5, distinct, obovate-oblong, 2–2.5 cm long, 5–10 mm wide, fleshy, glabrous, margin entire, apical one-quarter orange and basal three-quarters white.	3–5, usually oblong, 10–20 × 5–15 mm, slightly longer than sepals, abaxially glabrous, adaxially pubescent, base broadly saccate.
Stamen number	10–12	8–10	8–12
Filaments	Pubescent	Glabrous	Pubescent
Style	2–3 mm long; stigma funnel-shaped.	5–7 mm long; stigma funnel-shaped.	2–5 mm long; stigma funnel-shaped, often lead grey-blue and sparsely long-hairy.
Fruit	Capsule, erect at maturity.	Baccate fruit (berry), pedicel curved and nodding at maturity.	Berries erect to nodding, white, ovoid-globose.
Flowering period	June–October	March–June	April–August
Fruiting period	September–November	April–July	May–September

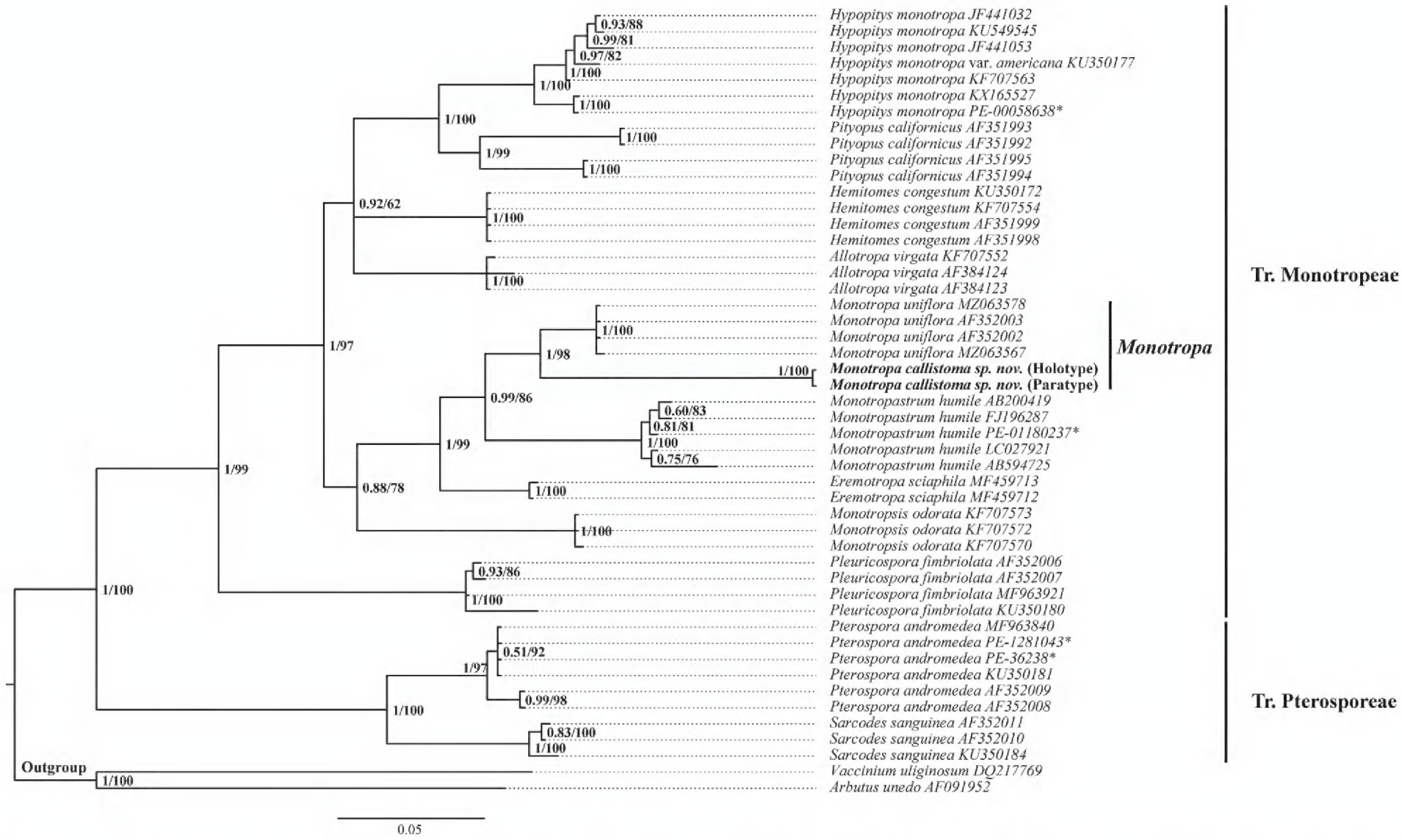

Figure 3. Majority-rule consensus tree from Bayesian Inference (BI), based on 49 nrITS sequences. Bayesian posterior probabilities (PP) and Maximum Likelihood (ML) bootstrap values (BS) are shown above the branches, respectively. New species are highlighted in bold, while other newly-sequenced sequences are marked with an asterisk (*).

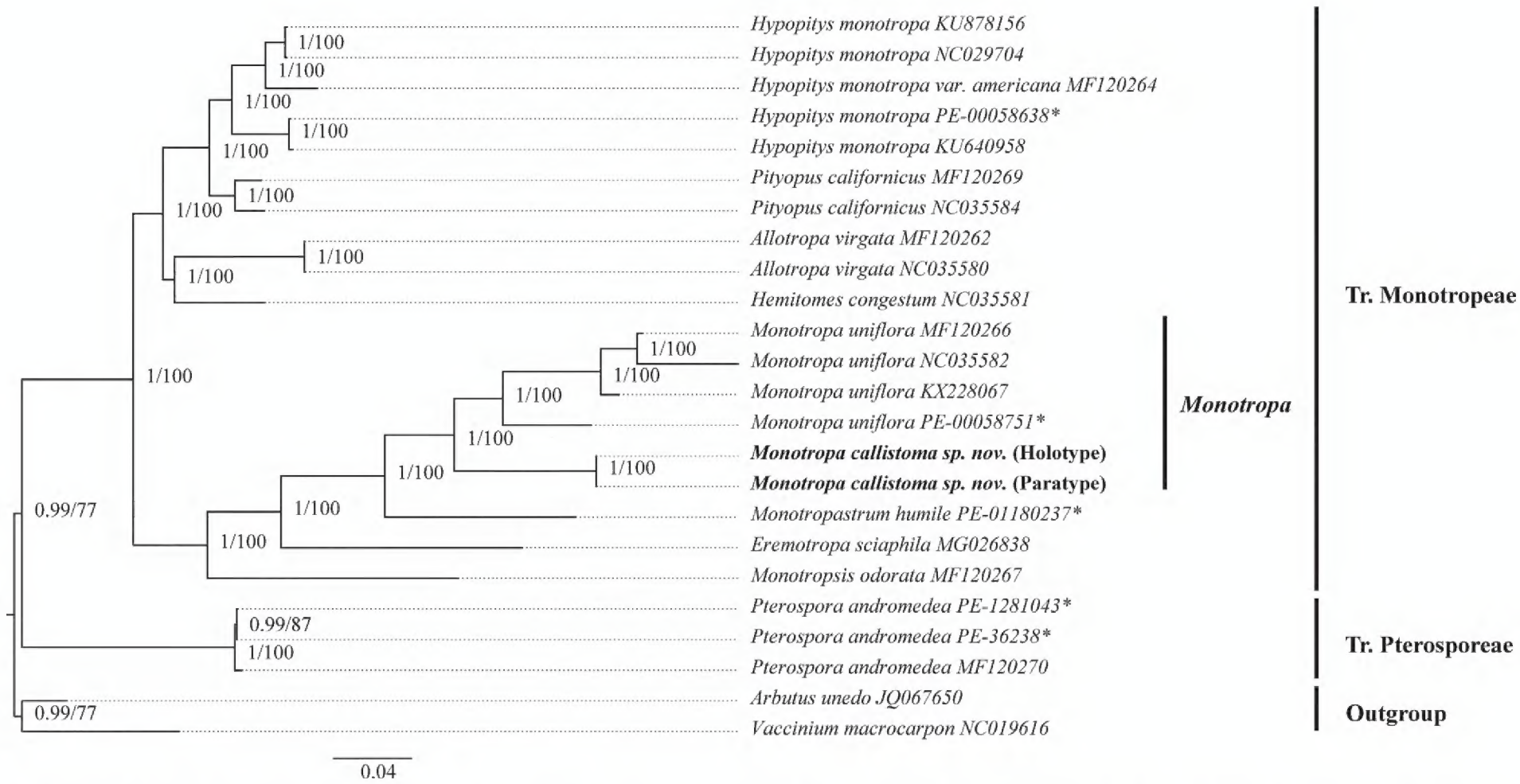

Figure 4. Majority-rule consensus tree from Bayesian Inference (BI), based on 23 single-copy coding sequences (CDSs) extracted from 24 chloroplast (cp) genomes. Bayesian posterior probabilities (PP) and Maximum Likelihood (ML) bootstrap values (BS) are shown above the branches, respectively. New species are highlighted in bold, while other newly-sequenced sequences are marked with an asterisk (*).

Table 3. Features of seven newly sequenced Monotropoideae plastomes.

Taxa	Voucher Specimen	Total length (bp)	GC content (%)	Gene numbers
Monotropa uniflora L.	PE00058751	42,959	28.5	47
Monotropa callistoma sp. nov.	PE02432009 (Paratype)	41,085	30.8	44
Monotropa callistoma sp. nov.	PE02432010 (Holotype)	41,041	30.8	44
Hypopitys monotropa Crantz	PE00058638	34,955	34	35
Monotropastrum humile (D. Don) H. Hara	PE01180237	40,507	30.6	43
Pterospora andromedea Nuttall	PE (Accession number pending, Sheet number 36238)	48,957	33.4	38
Pterospora andromedea Nuttall	PE (Accession number pending, Sheet number 1281043)	49,007	33.3	38

Discussion

Our integrative study, combining morphological observation, phylogenetic analysis and phenological investigation, provides evidence for the recognition of *Monotropa callistoma* as a new species. This discovery not only enriches the biodiversity of the genus *Monotropa*, but also offers fresh insights into the evolutionary dynamics and species delimitation within the enigmatic subfamily Monotropoideae.

The distinct morphological characters of *M. callistoma* provide the most direct evidence for its taxonomic distinction. The combination of 4–5 glabrous, bicoloured (apically orange and basally white) petals, 8–10 stamens with glabrous filaments and a nodding berry fruit at maturity is not found in any of the three previously known *Monotropa* species and two *Monotropastrum* species (Linnaeus 1753; Zuccarini 1832; Small 1927; Fang and Hu 1990; Luteyn et al. 1995; Klooster and Culley 2009; Suetsugu et al. 2023). Particularly, the petal colouration is a remarkable and previously unreported trait in these two genera. This suite of morphological differences is further solidified by a clear phenological barrier. The flowering period of *M. callistoma* (March–June) exhibits minimal overlap with that of its sister species, *M. uniflora* (June–October). This phenological isolation represents a potent pre-zygotic reproductive barrier, effectively preventing gene flow and facilitating independent evolutionary trajectories (Coyne and Orr 2004; Wang et al. 2021).

The baccate fruit of *M. callistoma*, however, prompts a deeper consideration of its generic placement. Unilocular ovaries, parietal placentation and baccate fruits are considered key characteristics distinguishing *Monotropastrum* from *Monotropa*, which typically bears capsules (Wallace 1987; Stevens et al. 2004; Qin and Wallace 2005; Tsukaya et al. 2008; Zhao et al. 2018). In this respect, *M. callistoma* aligns more closely with the definition of *Monotropastrum*. Nonetheless, incorporating *M. callistoma* into *Monotropastrum* would conflict with the current circumscription of the genus and its phylogenetic position, likely rendering *Monotropastrum* paraphyletic. Multiple evolutionary transitions from dry to fleshy fruits have occurred throughout angiosperm history, including at least 58 independent shifts from capsules to berries (Xiang et al. 2024). This suggests that fruit type may be a relatively labile trait. Additional characters, such as anther dehiscence patterns, have also been noted to differ between the genera (Hara 1966). Given the limited morphological research on many species within this group, generic boundaries remain somewhat ambiguous.

Considering the above and in light of the current incomplete sampling and morphological characterisation across the lineage, we adopt a conservative

and practical taxonomic approach. We tentatively place this new species within a broader (*sensu lato*) concept of the genus *Monotropa* and provisionally include *Monotropastrum humile* within this framework as well. We refrain from making formal nomenclatural recombinations at this time, pending future studies with expanded sampling and more comprehensive investigations of morphological and functional traits to definitively resolve the taxonomic relationships amongst these closely-related groups.

The robust support from both chloroplast genome and nrITS phylogenies confirms the genetic distinctness of *M. callistoma* (Figs 3, 4). Its consistent position as a well-supported monophyletic lineage sister to *M. uniflora* validates the morphological observations and confirms its placement within the genus *Monotropa*. Furthermore, our phylogenetic reconstructions corroborate recent taxonomic revisions concerning the monophyly of genera within Monotropoideae (Liu et al. 2017; Zhao et al. 2018; Freudenstein and Broe 2024). The clear resolution of the *Monotropa-Monotropastrum-Eremotropa-Monotropsis* clade provides a solid framework for understanding generic relationships within the tribe.

The highly reduced chloroplast genomes assembled in this study, including that of *M. callistoma*, are emblematic of the extreme evolutionary consequences of a fully mycoheterotrophic lifestyle. The extensive gene loss and size reduction observed (Table 3) align with the pattern widely documented in other non-photosynthetic plants (Lallemand et al. 2016; Logacheva et al. 2016; Braukmann et al. 2017; Liu et al. 2020; Suetsugu et al. 2024; Harada et al. 2025). This reductive evolution is driven by the relaxation of functional constraints on the photosynthetic apparatus and the translational machinery in the absence of light (Wicke and Naumann 2018). The persistence of a minimal plastome in *M. callistoma* and its relatives suggests that certain genes, likely those involved in essential non-photosynthetic functions, such as gene expression and possibly interactions with the mycorrhizal symbiont, are under purifying selection and are retained.

The discovery of *M. callistoma* in a well-botanised region of subtropical China underscores that the diversity of mycoheterotrophic plants may still be underestimated. Their cryptic nature, small size and ephemeral appearance above ground make them easily overlooked. Moreover, species complexes that are morphologically similar, but reproductively isolated by phenology or other subtle characters may be lumped under a single name (Rose and Freudenstein 2014; Freudenstein et al. 2016).

Conclusions

In conclusion, we describe *Monotropa callistoma* as a new species, based on a synthesis of multiple lines of evidence. This study demonstrates how the interplay of morphological specialisation, phenological shifts and genetic divergence can drive speciation even in lineages with highly reduced body plans. It also reinforces the notion that continued exploration and application of molecular tools are crucial for accurately documenting the true extent of plant diversity, particularly for inconspicuous and functionally specialised groups.

Taxonomic treatment

***Monotropa callistoma* Ze Wei, Li J.Liu & Bing Liu, sp. nov.**
urn:lsid:ipni.org:names:77371852-1
Figs 1, 2, 6

Diagnosis. *Monotropa callistoma* is characterised by its 4 or 5 glabrous petals (apically orange and basally white), 8–10 stamens with glabrous filaments, flowering period starting from March and nodding capsule at maturity. It is morphologically most similar to *M. uniflora* and *Monotropastrum humile*, but differs by the characters summarised in Table 2.

Type. CHINA. • Hunan Province: Shaoyang City, Xinning County, Shunhuang Mountain, 1560 m elev., 29 March 2021, *Xuan Jing, Xie Gan, Wei Ze & Ouyang Wenxiang 60* (holotype: PE [PE02432010!]) (Fig. 5)

Figure 5. Type of *Monotropa uniflora* (Holotype PE02432010).

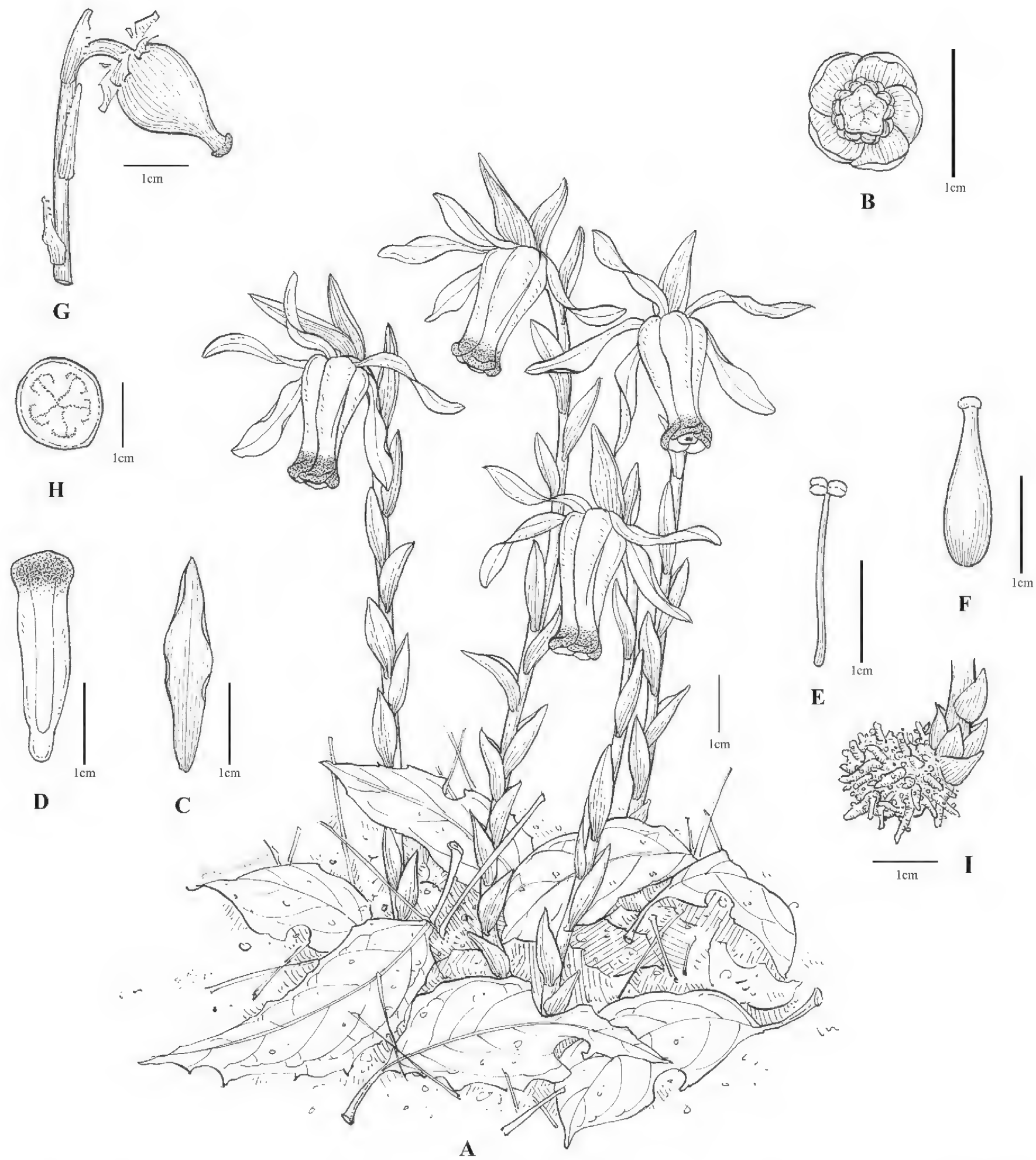

Figure 6. *Monotropa callistoma* sp. nov. **A.** Habitat and flowering plant; **B.** Flower, viewed from the top; **C.** Sepal; **D.** Petal; **E.** Stamen; **F.** Pistil; **G.** Berry; **H.** Transverse section of the berry fruit showing the parietal placentation; **I.** Mycorrhiza. Drawn by Yi F. Li.

Description. Herbs, fully mycoheterotrophic. Plants lacking chlorophyll, white when fresh, turning black upon drying. Stems erect, simple, unbranched, 9–15 cm tall, fleshy. Roots thick, densely branched, forming a bird's-nest-like mass. Leaves scale-like, erect, alternate, oblong to broadly lanceolate, 12–18 mm long, 4–6.5 mm wide, apex obtuse, glabrous, margin nearly entire. Flower solitary, terminal, campanulate, 2–3 cm long, 1–1.5 cm in diameter. Sepals 4 or 5, scale-like. Petals 4 or 5, distinct, obovate-oblong, 2–2.5 cm long, 5–10 mm wide, fleshy, glabrous, orange in the apical one-quarter and white in the basal three-quarters, margin entire. Stamens 8–10; filaments glabrous; anthers yellow. Ovary glabrous, with parietal placentation, 1-loculed; style

5–7 mm long; stigma expanded, funnel-shaped. Berries ellipsoid-globose, with the fruiting pedicel becoming curved and nodding at maturity.

Phenology. Flowering from March to June; fruiting from April to July.

Distribution and habitat. Currently known only from the type locality in Hunan Province, China. It grows in dense, humid broad-leaved forests at an elevation of around 1560 m, in association with ectomycorrhizal fungi. However, according to records from PPBC (https://ppbc.iplant.cn/) and iNaturalist (www.inaturalist.org/), it has also been reported from Guizhou, Yunnan, Guangxi, Sichuan, Hunan, Xizang and Chongqing. As these records are based solely on photographs without supporting herbarium specimens, they are considered unverified and serve only as references.

Vernacular name (Chinese name). 美冠水晶兰 (měi guān shuǐ jīng lán).

Etymology. The specific epithet *callistoma* is derived from the Greek *calli-* (beautiful) and *-stoma* (mouth), alluding to the aesthetically pleasing form and colouration of the corolla orifice.

Preliminary conservation status. Data Deficient (DD). This species is currently known only from a single population. Further field surveys are needed to assess its full distribution and population size. The type locality is within a protected scenic area, which may offer some level of protection.

Additional specimens examined (Paratype). CHINA. • Hunan Province: Shaoyang City, Xinning County, Shunhuang Mountain, 1560 m elev., 29 March 2021, Xuan Jing, Xie Gan, Wei Ze & Ouyang Wenxiang 60 (PE024320009!).

Key to the species of *Monotropa* s.l. (*Monotropa* s.s. & *Monotropastrum*)

1 Berry, pendulous at maturity; sepals persistent **2**
– Capsule, erect at maturity; sepals deciduous **4**
2 Filaments, style and petals glabrous; flower apex orange ..... ***Monotropa callistoma***
– Filaments, style and inner surface of petals pubescent; flowers white or pink **3**
3 Tepals white; sepals (2–)3–5, oblong, spreading at anthesis ..... ***Monotropastrum humile***
– Tepals rosy pink; sepals 4–11, elliptic, constantly appressed to the petals throughout anthesis ..... ***Monotropastrum kirishimense***
4 Plant entirely glabrous, bright red ..... ***Monotropa coccinea***
– Filaments and inner surface of petals densely pubescent; flowers greenish-yellow, ochroleucous or white **5**
5 Sepals and petals not ciliate at margins; capsule 0.5–1.2(–1.4) cm long ..... ***Monotropa uniflora***
– Sepals and petals ciliate at margins, shallowly saccate at base; capsule larger, 1.5–2 cm long ..... ***Monotropa brittonii***

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Q W, M L and B L designed the research. Z W, J X, ZQ M and WX OY collected the data; LJ L and Z W analysed the data; LJ L and Z W prepared the manuscript. All authors read and approved the final manuscript.

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Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

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Supplementary material 1

Supplementary tables

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Data type: xlsx

Explanation note: **table S1.** Taxa newly sequenced in the present study with source, voucher and GenBank accession numbers. **table S2.** Newly sequenced data in this study.

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